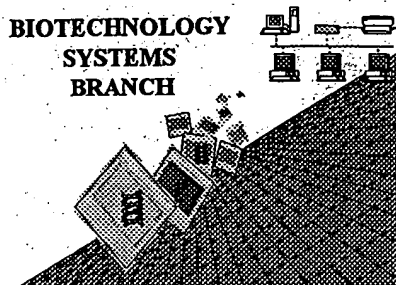


RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/431,843

Art Unit / Team No. :

OIR

Date Processed by STIC:

11/18/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/431,843

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☒ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)
- 12 ☐ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

SEQ ID

1 rat OGFr cDNA
5 2 rat OGFr protein
3 rat OGFr cDNA partial (clone 14)
4 human OGFr cDNA (Provisional)
5 human OGFr splice version 8, cDNA
6 human OGFr splice version 8, protein
10 7 human OGFr splice version 1, cDNA
8 human OGFr splice version 1, protein
9 human OGFr splice version 4, cDNA
10 human OGFr splice version 4, protein
11 human OGFr splice version 7, cDNA
15 12 human OGFr splice version 7, protein
13 human OGFr splice version 127, cDNA
14 human OGFr splice version 127, protein
15 rat OGFr antisense 5'-GACTCAGGGACTTAGCTTCATCC-3'
20 16 scrambled 5'-ATAGATACTACGCCGGCTGTCCT-3'
17 human OGFr antisense 5'-GGTCGTCCATGCTCGGCTAGAAT-3'
18 scrambled 5'-GTGCAGTGCAATGCTCTCCGTGA-3'

25

SEQ ID NO: 1 -- Rat Opioid Growth Factor Receptor cDNA sequence

TGGGCTCAGCCACGCCCCAGGGTGCCCCAGTGGGACTAGTTCTTCATTCTGGCAGCTGCACACATCTGTCAGTG
30 AGGGAATGTCAGGTC 90
TCTCACTCTCCTCTCCTCACTATCCTTTCCGCAGAAAGCGGGTCTCCTGCTTGTGCGAGTATGGACGACCCGGACT
GCGATTCCACCTGG 180
GAGGAGGAGAGCGAGGAGGATGGCGAGGATGGCCAGGCGGATGATACGACCGATGAGGACACGGGCGACGAT
GACGGCGACGCGGAGGAG 270
35 GCACGGCCAAGCCTGTTCCAGTCCAGGATGACAGGGTACCGAACTGGCGTGCTATGCAGGACATGCAAAGATA
CCGGCACAACCTACCCG 360
GATTGACAGATCAAGACTGCAATGGTGACATGTGCAACCTGAGCTTCTACAAAATGAGATCTGCTTCCAGCCAA
ATGGGGCTCTCATC 450
GAGGACATTCTTCAGAACTGGAAAGACAACCTATGACCTCCTGGAAGAGAATCACTCCTACATCCAGTGGCTGTTTC
40 CTCTGCGGGAACCA 540
GGAGTGAAGTGGCACGCCAAGCCCCTCACCCTGAAGGAGGTTGAGGCATTTAAAGCTCCAAGGAAGTCAGAGA
GCGTCTTGTCCGGGCC 630
TATGAGCTCATGCTGGGCTTCTATGGGTTCCACCTTGAGGACCGGGGCACGGGTGCTGTATGCCGTGCACAGAA
CTTCCAGCCGCGCTTC 720
45 CACAATCTGAACAGCCACAGCCACAACAACCTGCGTATTACACGCATCCTCAAGTCACTGGGTGAGCTGGGCTTA
GAACACTACCAGGCA 810

09/43,843

filename: 1984se~1.rtf

Does Not Comply
Corrected Diskette Needed

Partial listing of
submitted file. This
is completely invalid
format for a sequence
Listing. Please:

1) consult new
sequence Rules for
valid format
2) see
sample
sequence
Listing,
attached, for
valid
format.

also,
please
see
item 5
on Error
summary
sheet

Appendix A To Subpart G to Part 1—Sample Sequence Listing

<110> Smith, John

Smith, Jane

<120> Example of a Sequence Listing

<130> 01-00001

<140> US 08/999,999

<141> 1998-02-28

<150> EP 91000000

<151> 1997-12-31

Please consult

<160> 2

<170> PatentIn ver. 2.0

<210> 1

<211> 403

<212> DNA

<213> Paramecium aurelia

<220>

<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a

Protease from Paramecium sp.

<303> Journal of Fictional Genes

<304> 1

<305> 4

<306> 1 - 7

<307> 1988-06-20

<400> 1

ctactctact ctactctcat ctactatctt ctttggatct ctgagtctgc ctgagtggta 60

ctcttgagtc ctggagatct ctctctcac atgtgatcgt cgagactgac cgatagatcg 120

ctgactgact ctgagatagt cgagcccgta cgagaccgt cgagggtgac agagagtggg 180

cgcggtgcgcg cagagcgccg cgccggtgcg cgcgcgagtg cgcggtgggc cgcgcgaggg 240

ctttcgcggc agcggcggcg ctttcggcg cgcgccgctc cgccctaga cctgagaggt 300

cttctcttcc ctctcttca ctagagaggt ctatatatac atg gtt tca atg ttc 355

Met Val Ser Met Phe

agc ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgtttgctc 403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

- 10

15

<210> 2

<211> 18

<212> PRT

<213> Paramecium aurelia

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1

5

10

15

Phe Val

ed: May 22, 1998.

A. Lehman,

ant Secretary of Commerce and
Commissioner of Patents and Trademarks.

oc. 98-14194 Filed 5-29-98; 8:45 am]

1 CODE 3510-16-C

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;